

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 1c/004,201

CRF Processing Date: 4/5/2002
 Edited by: AS
 Verified by: AS (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:

- ☐ Deleted extra, invalid, headings used by an applicant, specifically:

- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically:

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other:

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**



OIPE

RAW SEQUENCE LISTING

DATE: 04/05/2002

PATENT APPLICATION: US/10/004,201

TIME: 19:41:27

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\04052002\J004201.raw

p.6

```

4 <110> APPLICANT: Bornaes, Claus
5     Andersen, Kim Vilbour
6     Rasmussen, Poul Baad
7     Pedersen, Anders Hjelholt
10 <120> TITLE OF INVENTION: NEW MULTIMERIC INTERFERON BETA
11     POLYPEPTIDES
13 <130> FILE REFERENCE: 0220us210
15 <140> CURRENT APPLICATION NUMBER: US 10/004,201
C--> 16 <141> CURRENT FILING DATE: 2002-03-19
18 <150> PRIOR APPLICATION NUMBER: US 60/245,645
19 <151> PRIOR FILING DATE: 2000-11-02
21 <160> NUMBER OF SEQ ID NOS: 39
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 840
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (76)...(636)
34 <221> NAME/KEY: sig_peptide
35 <222> LOCATION: (76)...(138)
W--> 37 <221> mat_peptide
38 <222> LOCATION: (139)...(636)
W--> 40 <400> 1
41 acattctaac tgcaaccttt cgaagccttt gctctggcac aacaggtagt aggcgacact 60
42 gttcgtgttg tcaac atg acc aac aag tgt ctc ctc caa att gct ctc ctg 111
43           Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu
44           -20           -15           -10
46 ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga 159
47 Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly
48           -5           1           5
50 ttc cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa 207
51 Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln
52           10           15           20
54 ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac 255
55 Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp
56           25           30           35
58 atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc 303
59 Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala
60 40           45           50           55
62 gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga 351
63 Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg

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64          60          65          70
66 caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc 399
67 Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu
68          75          80          85
70 ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa 447
71 Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu
72          90          95          100
74 gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt 495
75 Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser
76          105          110          115
78 ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc 543
79 Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala
80 120          125          130          135
82 aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta 591
83 Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu
84          140          145          150
86 agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac 636
87 Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
88          155          160          165
90 tgaagatctc ctagcctgtg cctctgggac tggacaattg cttcaagcat tcttcaacca 696
91 gcagatgctg tttaagtgc tgatggctaa tgtactgcat atgaaaggac actagaagat 756
92 tttgaaattt ttattaaatt atgagttatt tttattttatt taaattttat tttggaaaat 816
93 aaattatttt tggtgcaaaa gtca 840
95 <210> SEQ ID NO: 2
96 <211> LENGTH: 187
97 <212> TYPE: PRT
98 <213> ORGANISM: Homo sapiens
100 <220> FEATURE:
101 <221> NAME/KEY: SIGNAL
102 <222> LOCATION: (1)...(21)
104 <221> NAME/KEY: CHAIN
105 <222> LOCATION: (22)...(187)
W--> 107 <400> 2
108 Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
109 -20 -15 -10
110 Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
111 -5 1 5 10
112 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
113 15 20 25
114 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
115 30 35 40
116 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
117 45 50 55
118 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
119 60 65 70 75
120 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
121 80 85 90
122 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
123 95 100 105

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124 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
125          110          115          120
126 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
127          125          130          135
128 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
129 140          145          150          155
130 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
131          160          165
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 614
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Synthetic construct
W--> 142 <221> NAME/KEY: CDS
143 <222> LOCATION: (25)...(585)
W--> 145 <221> sig_peptide
146 <222> LOCATION: (25)...(87)
W--> 148 <221> mat_peptide
149 <222> LOCATION: (88)...(585)
W--> 151 <400> 3
152 cgtttaaact taagcttcgc cacc atg acc aac aag tgc ctg ctc cag atc 51
153          Met Thr Asn Lys Cys Leu Leu Gln Ile
154          -20          -15
156 gcc ctg ctc ctg tgc ttc agc acc acg gcc cta tcg atg agc tac aac 99
157 Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn
158          -10          -5          1
160 ctg ctc ggc ttc ctg cag agg agt tcg aac ttc cag tgc cag aag ctc 147
161 Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu
162 5          10          15          20
164 ctg tgg cag ctg aac ggg cgc ctg gag tac tgc ctg aag gac agg atg 195
165 Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met
166          25          30          35
168 aac ttc gac atc ccc gag gaa atc aag cag ctg cag cag ttc cag aag 243
169 Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys
170          40          45          50
172 gag gac gcc gct ctg acc atc tac gag atg ctg cag aac atc ttc gcc 291
173 Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala
174          55          60          65
176 atc ttc cgc cag gac tcc agc tcc acc ggt tgg aac gag acc atc gtg 339
177 Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val
178          70          75          80
180 gag aac ctg ctg gcc aac gtg tac cac cag atc aac cac ctg aag acc 387
181 Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr
182 85          90          95          100
184 gtg ctg gag gag aag ctg gag aag gag gac ttc acc cgc ggc aag ctg 435
185 Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu
186          105          110          115
188 atg agc tcc ctg cac ctg aag cgc tac tat ggc cgc atc ctg cac tac 483

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189 Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr
190          120          125          130
192 ctg aag gcc aag gag tac agc cac tgc gcc tgg acc atc gta cgc gtg   531
193 Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val
194          135          140          145
196 gag atc ctg cgc aac ttc tac ttc atc aac cgc ctg acc ggc tac ctg   579
197 Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu
198          150          155          160
200 cgc aac tgataaggat ccactagttcc agtgtggtg   614
201 Arg Asn
202 165
205 <210> SEQ ID NO: 4
206 <211> LENGTH: 4
207 <212> TYPE: PRT
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: Synthetic construct
W--> 213 <221> NAME/KEY: VARIANT
214 <222> LOCATION: 4
215 <223> OTHER INFORMATION: Xaa = Thr or Ser
W-1> 217 <400> 4
W-1> 218 Ile Asn Ala Xaa
219 1
222 <210> SEQ ID NO: 5
223 <211> LENGTH: 4
224 <212> TYPE: PRT
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Synthetic construct
W--> 230 <221> NAME/KEY: VARIANT
231 <222> LOCATION: 4
232 <223> OTHER INFORMATION: Xaa = Thr or Ser
W-1> 234 <400> 5
W-1> 235 Gly Asn Ile Xaa
236 1
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 4
241 <212> TYPE: PRT
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Synthetic construct
W--> 247 <221> NAME/KEY: VARIANT
248 <222> LOCATION: 4
249 <223> OTHER INFORMATION: Xaa = Thr or Ser
W-1> 251 <400> 6
W-1> 252 Val Asn Ile Xaa
253 1
256 <210> SEQ ID NO: 7
257 <211> LENGTH: 4

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258 <212> TYPE: PRT
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Synthetic construct
W--> 264 <221> NAME/KEY: VARIANT
265 <222> LOCATION: 4
266 <223> OTHER INFORMATION: Xaa = Thr or Ser
W-H- 268 <400> 7
W-H- 269 Ser Asn Ile Xaa
270 1
273 <210> SEQ ID NO: 8
274 <211> LENGTH: 5
275 <212> TYPE: PRT
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Synthetic construct
W--> 281 <221> NAME/KEY: VARIANT
282 <222> LOCATION: 5
283 <223> OTHER INFORMATION: Xaa = Thr or Ser
W-H- 285 <400> 8
W-H- 286 Ala Ser Asn Ile Xaa
287 1 5
290 <210> SEQ ID NO: 9
291 <211> LENGTH: 6
292 <212> TYPE: PRT
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
296 <223> OTHER INFORMATION: Synthetic construct
W--> 298 <221> NAME/KEY: VARIANT
299 <222> LOCATION: 6
300 <223> OTHER INFORMATION: Xaa = Thr or Ser
W-H- 302 <400> 9
W-H- 303 Ser Pro Ile Asn Ala Xaa
304 1 5
307 <210> SEQ ID NO: 10
308 <211> LENGTH: 7
309 <212> TYPE: PRT
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Synthetic construct
W--> 315 <221> NAME/KEY: VARIANT
316 <222> LOCATION: 7
317 <223> OTHER INFORMATION: Xaa = Thr or Ser
W-H- 319 <400> 10
W-H- 320 Ala Ser Pro Ile Asn Ala Xaa
321 1 5
324 <210> SEQ ID NO: 11
325 <211> LENGTH: 11
326 <212> TYPE: PRT

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/004,201

DATE: 04/05/2002
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Input Set : A:\PTO.AMC.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 4
Seq#:5; Xaa Pos. 4
Seq#:6; Xaa Pos. 4
Seq#:7; Xaa Pos. 4
Seq#:8; Xaa Pos. 5
Seq#:9; Xaa Pos. 6
Seq#:10; Xaa Pos. 7
Seq#:11; Xaa Pos. 4,8
Seq#:12; Xaa Pos. 4,9,14